

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 10:18:03 ; Search time 17609 Seconds
(without alignments)
11497.390 Million cell updates/sec

Title: US-10-501-930-2
Perfect score: 3166
Sequence: 1 cggagcggcgagtcggtgcc.....gctattagcaaaaaaaaaaaa 3166

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
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9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query			Description
Result	No.	Score	Match	Length	DB	ID	
	1	3166	100.0	3166	6	AB059554	AB059554 Mus muscu
c	2	2361	74.6	110000	12	BX322642_0	BX322642 Mus muscu
	3	2361	74.6	110000	12	BX322642_2	Continuation (3 of
c	4	2361	74.6	110000	12	BX322642_2	Continuation (3 of
c	5	2361	74.6	202001	6	AL772303	AL772303 Mouse DNA
	6	1408.4	44.5	236283	12	AC120773	AC120773 Rattus no
c	7	1408.4	44.5	264245	12	AC096804	AC096804 Rattus no

8	1028	32.5	1197	6	AJ699423	AJ699423 Rattus no
9	861.8	27.2	1234	5	AJ621583	AJ621583 Homo sapi
10	857.8	27.1	1197	5	AJ697663	AJ697663 Pan trogl
11	757	23.9	1197	14	AJ868431	AJ868431 Bos tauru
12	559.8	17.7	1149	2	CQ736679	CQ736679 Sequence
c 13	470.4	14.9	151289	5	AL158164	AL158164 Human DNA
14	467.2	14.8	1197	11	AJ699424	AJ699424 Gallus ga
15	456.8	14.4	1520	11	CR352448	CR352448 Gallus ga
16	381	12.0	112099	12	AC143457	AC143457 Macaca mu
17	257.8	8.1	493	7	BV211170	BV211170 SIAT8F_5
18	256.6	8.1	1334	11	AJ704564	AJ704564 Gallus ga
19	248.2	7.8	1140	11	AJ715548	AJ715548 Tetraodon
20	247.6	7.8	1131	6	AJ699422	AJ699422 Rattus no
21	244	7.7	1131	5	AJ697662	AJ697662 Pan trogl
22	244	7.7	1131	5	CR457037	CR457037 Homo sapi
23	244	7.7	1878	2	CQ721379	CQ721379 Sequence
24	244	7.7	1953	5	BC108910	BC108910 Homo sapi
25	244	7.7	1953	5	BC108911	BC108911 Homo sapi
26	242.8	7.7	1881	6	BC034855	BC034855 Mus muscu
27	242.4	7.7	2594	5	AK056270	AK056270 Homo sapi
28	241.2	7.6	1854	6	MMA28ST	X98014 M.musculus
29	239.2	7.6	1899	5	HSU91641	U91641 Human alpha
30	237.8	7.5	2135	5	AK094273	AK094273 Homo sapi
31	234.4	7.4	1125	14	AJ868432	AJ868432 Bos tauru
32	231.6	7.3	2094	5	AK130126	AK130126 Homo sapi
33	228.8	7.2	1032	11	AJ715546	AJ715546 Danio rer
34	228.2	7.2	1137	11	AJ871609	AJ871609 Oryzias l
35	224.4	7.1	1071	2	AX481522	AX481522 Sequence
36	224.4	7.1	1630	5	HUMGD3G	L43494 Human gangl
37	224.4	7.1	1704	5	HUMGD3S	D26360 Homo sapien
38	224.4	7.1	1755	2	CQ721891	CQ721891 Sequence
39	224.4	7.1	2117	2	AR360634	AR360634 Sequence
40	224.4	7.1	2117	5	HSGD3S	X77922 H.sapiens G
41	222.8	7.0	1650	5	HUM28SIATR	L32867 Homo sapien
42	221.2	7.0	1071	5	AJ697658	AJ697658 Pan trogl
43	220.4	7.0	1116	11	AJ705092	AJ705092 Takifugu
44	220.4	7.0	1140	11	AJ715547	AJ715547 Takifugu
45	211.6	6.7	2381	6	BC024821	BC024821 Mus muscu

ALIGNMENTS

RESULT 1

AB059554

LOCUS AB059554 3166 bp mRNA linear ROD 27-APR-2005

DEFINITION Mus musculus ST8Sia VI mRNA for alpha 2,8-sialyltransferase, complete cds.

ACCESSION AB059554

VERSION AB059554.1 GI:21668466

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Takashima,S., Ishida,H.K., Inazu,T., Ando,T., Ishida,H., Kiso,M., Tsuji,S. and Tsujimoto,M.

TITLE Molecular cloning and expression of a sixth type of alpha 2,8-sialyltransferase (ST8Sia VI) that sialylates O-glycans

JOURNAL J. Biol. Chem. 277 (27), 24030-24038 (2002)
PUBMED 11980897
REFERENCE 2 (bases 1 to 3166)
AUTHORS Takashima,S.
TITLE Direct Submission
JOURNAL Submitted (07-APR-2001) Shou Takashima, RIKEN, Cellular
Biochemistry Laboratory; 2-1 Hirosawa, Wako, Saitama, 351-0198,
Japan (E-mail:staka@riken.jp, Tel:81-48-462-1111(ex.3424),
Fax:81-48-462-4670)
FEATURES Location/Qualifiers
source 1. .3166
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/country="Japan"
gene 1. .3166
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CDS 77. .1273
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CENVKLYGFWPFSKTIEDTPLSHHYDNLMLPKHGFHQMPKEYSQMLQLHMRGILKLQF
SKCETA"

ORIGIN

Query Match 100.0%; Score 3166; DB 6; Length 3166;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CGGAGCGGCGAGTCGGTGCCGCCCGGGCTGCGCTTCGCCCCGGCAGCTTTGGCGGCGAGG	60
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Qy	61	ACGCCCCTGGCTCAGGATGAGATCGGGGGGCACGCTGTTCGCCCTCATAGGCAGCCTGAT	120
Db	61	ACGCCCCTGGCTCAGGATGAGATCGGGGGGCACGCTGTTCGCCCTCATAGGCAGCCTGAT	120
Qy	121	GCTGCTGCTCCTCCTGCGTATGCTCTGGTGCCCGACCGCGCCTGCCCGCTCCAGGCT	180
Db	121	GCTGCTGCTCCTCCTGCGTATGCTCTGGTGCCCGACCGCGCCTGCCCGCTCCAGGCT	180
Qy	181	GTTGATGGAGGGAAGCAGAGAGGACACCAAGTGGTACCTCAGCTGCACTGAAGACACTCTG	240
Db	181	GTTGATGGAGGGAAGCAGAGAGGACACCAAGTGGTACCTCAGCTGCACTGAAGACACTCTG	240
Qy	241	GAGCCCGACAACCCCGGTACCACGCACCAGGAACAGCACATATCTGGATGAGAAGACAAC	300
Db	241	GAGCCCGACAACCCCGGTACCACGCACCAGGAACAGCACATATCTGGATGAGAAGACAAC	300
Qy	301	CCAAATAACAGAGAAATGCAAAGATCTGCAATATAGCTTGAACCTCTTTATCTAACAAAAC	360
Db	301	CCAAATAACAGAGAAATGCAAAGATCTGCAATATAGCTTGAACCTCTTTATCTAACAAAAC	360

Qy	361	GAGACGGTACTCTGAGGATGACTACCTCCAGACCATCACAAACATACAGAGATGCCCATG	420
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Qy	421	GAACCGGCAAGCAGAAGAATATGACAATTTTAGAGCAAACTGGCTTCCTGTTGCGATGC	480
Db	421	GAACCGGCAAGCAGAAGAATATGACAATTTTAGAGCAAACTGGCTTCCTGTTGCGATGC	480
Qy	481	CATTCAAGACTTCGTGGTTTCCCAGAACAACACTCCAGTGGGGACTAACATGAGCTACGA	540
Db	481	CATTCAAGACTTCGTGGTTTCCCAGAACAACACTCCAGTGGGGACTAACATGAGCTACGA	540
Qy	541	GGTGGAAGCAAGAAACACATCCCCATTCGAGAGAACATTTTCCACATGTTTCCAGTGTC	600
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Db	601	GCAGCCTTTTGTGGACTATCCCTATAACCAGTGTGCAGTGGTTGGTAATGGGGGAATTCT	660
Qy	661	CAACAAGTCTCTCTGCGGAGCAGAAATTGATAAATCTGACTTCGTCTTCAGGTGTAACT	720
Db	661	CAACAAGTCTCTCTGCGGAGCAGAAATTGATAAATCTGACTTCGTCTTCAGGTGTAACT	720
Qy	721	CCCCCAATCACAGGGAGCGCTAGTAAAGATGTTGGAAGCAAACAAATCTTGTGACTGT	780
Db	721	CCCCCAATCACAGGGAGCGCTAGTAAAGATGTTGGAAGCAAACAAATCTTGTGACTGT	780
Qy	781	CAATCCCAGCATTATAACCCTGAAGTACCAGAATTTGAAGGAGAAGAAAGCACAGTTTTT	840
Db	781	CAATCCCAGCATTATAACCCTGAAGTACCAGAATTTGAAGGAGAAGAAAGCACAGTTTTT	840
Qy	841	GGAGGACATCTCCACCTATGGAGATGCATTCTCTCCTGCCAGCATTTTCCTATCGGGC	900
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Db	901	CAACACAGGCATCTCTTTTAAAGTCTACCAAACACTCAAAGAGTCAAAAATGAGGCAAAA	960
Qy	961	GGTTCTCTTCTTCCATCCCAGGTACCTGAGACACCTCGCTCTTTTCTGGAGAACTAAAGG	1020
Db	961	GGTTCTCTTCTTCCATCCCAGGTACCTGAGACACCTCGCTCTTTTCTGGAGAACTAAAGG	1020
Qy	1021	GGTGACTGCATACCGCTTGTCCACAGGCTTGATGATTGCAAGTGTGCTGTGGAACGTGTG	1080
Db	1021	GGTGACTGCATACCGCTTGTCCACAGGCTTGATGATTGCAAGTGTGCTGTGGAACGTGTG	1080
Qy	1081	TGAAAACGTGAAGCTCTACGGATTCTGGCCTTTCTCTAAGACTATCGAAGACACCCCACT	1140
Db	1081	TGAAAACGTGAAGCTCTACGGATTCTGGCCTTTCTCTAAGACTATCGAAGACACCCCACT	1140
Qy	1141	CAGTCACCACTACTATGATAACATGTTACCTAAGCATGGTTTCCACCAGATGCCTAAAGA	1200
Db	1141	CAGTCACCACTACTATGATAACATGTTACCTAAGCATGGTTTCCACCAGATGCCTAAAGA	1200
Qy	1201	ATACAGCCAAATGCTCCAGCTCCATATGAGAGGAATCCTCAAACCTGCAATTCAGCAAATG	1260
Db	1201	ATACAGCCAAATGCTCCAGCTCCATATGAGAGGAATCCTCAAACCTGCAATTCAGCAAATG	1260
Qy	1261	TGAAACGGCTTAACGTTTCTTAGAAGGAGAATAATTTTCAGGAGGTGGAGTGGATGTGTCA	1320

Db	1261	 TGAAACGGCTTAACGTTTCTTAGAAGGAGAATAATTTTCAGGAGGTGGAGTGGATGTGTCA	1320
Qy	1321	CAGCATCTCCAAAAAGCCAATAGAAGAAGGCACAGAGAAAGCATGAATTACAAAGGCGCT	1380
Db	1321	 CAGCATCTCCAAAAAGCCAATAGAAGAAGGCACAGAGAAAGCATGAATTACAAAGGCGCT	1380
Qy	1381	CTCCCACTTGTCTAGACCAAAGCCACCCGCCCCACTCACTTTGCAGCCTCCACGAGTCA	1440
Db	1381	 CTCCCACTTGTCTAGACCAAAGCCACCCGCCCCACTCACTTTGCAGCCTCCACGAGTCA	1440
Qy	1441	CTCATTCTCACCTTCAACGTTCTTTCTCTGAGAATAGAGACCAAACATCAGACTTGGAT	1500
Db	1441	 CTCATTCTCACCTTCAACGTTCTTTCTCTGAGAATAGAGACCAAACATCAGACTTGGAT	1500
Qy	1501	AAGTAAATGAGATAATTTTTCAAATCATCATAGAATTTGATTTGAGCCAGGGTCTCTCA	1560
Db	1501	 AAGTAAATGAGATAATTTTTCAAATCATCATAGAATTTGATTTGAGCCAGGGTCTCTCA	1560
Qy	1561	GAATGCTTCCTTGTTCCTATCCATGATAGCCATTCCCACCTTTATCAGAGTGGTAATGAA	1620
Db	1561	 GAATGCTTCCTTGTTCCTATCCATGATAGCCATTCCCACCTTTATCAGAGTGGTAATGAA	1620
Qy	1621	ACTGTGCAATTGTGCCAAAGACCCTTTCTGAAGAGAATGTCTGAATCATGCGCCGAGTTT	1680
Db	1621	 ACTGTGCAATTGTGCCAAAGACCCTTTCTGAAGAGAATGTCTGAATCATGCGCCGAGTTT	1680
Qy	1681	TTACACACAGCTCTTCCTTTATAAATAAATCCTTCCCATTCTCCCTCCTAGTAGAGTACA	1740
Db	1681	 TTACACACAGCTCTTCCTTTATAAATAAATCCTTCCCATTCTCCCTCCTAGTAGAGTACA	1740
Qy	1741	GAAACAAAATACCCTTGATGATTCAGGAAGAAAAGTCTTTTTTACTTAGCAATGTGCCTG	1800
Db	1741	 GAAACAAAATACCCTTGATGATTCAGGAAGAAAAGTCTTTTTTACTTAGCAATGTGCCTG	1800
Qy	1801	CTTCTGATTCACTTCGCTTGTGACATTAAGCTGGGTGGGGTTTGGTTGGATTGGGGC	1860
Db	1801	 CTTCTGATTCACTTCGCTTGTGACATTAAGCTGGGTGGGGTTTGGTTGGATTGGGGC	1860
Qy	1861	GTTTCTTCACTTCTTTTGTCTATATTTTCCTTACCTTTATCAGTTTGTATTCGAGCTTCC	1920
Db	1861	 GTTTCTTCACTTCTTTTGTCTATATTTTCCTTACCTTTATCAGTTTGTATTCGAGCTTCC	1920
Qy	1921	TGCTTTGGGATTCTGCAATTCTCTCTCCCACTGACAGGATCAACTCAATGACATAAAGTA	1980
Db	1921	 TGCTTTGGGATTCTGCAATTCTCTCTCCCACTGACAGGATCAACTCAATGACATAAAGTA	1980
Qy	1981	GTTCAAACATCCATTGCTTCTCACATGTTTTATCCATAAAGTTACTCATCTGATTTTATT	2040
Db	1981	 GTTCAAACATCCATTGCTTCTCACATGTTTTATCCATAAAGTTACTCATCTGATTTTATT	2040
Qy	2041	TAAAATAGTGAACATCTACTTGATATCAGACCCGAGGACCATCCTCCATTGGAGAATATG	2100
Db	2041	 TAAAATAGTGAACATCTACTTGATATCAGACCCGAGGACCATCCTCCATTGGAGAATATG	2100
Qy	2101	AAGATATTGTCACTGGCAGAAAAGCAGGTGTGTGCCATTAATTGATAAGATACCACAAGC	2160
Db	2101	 AAGATATTGTCACTGGCAGAAAAGCAGGTGTGTGCCATTAATTGATAAGATACCACAAGC	2160
Qy	2161	ATCATCATGCCAGTTATGAACACAGTGCTGAAAGGATCATAGACAGGGTGGTTAAATCT	2220

Db	2161	ATCATCATGCCAGTTATGAACACAGTGCTGAAAGGATCATAGACAGGGGTGGTTAAATCT	2220
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Qy	2281	AACTAGTAAATGAACCAATTCTTAGGCACATTAAGTGGATTCTGAGTAAAAGAAAGGGAA	2340
Db	2281	AACTAGTAAATGAACCAATTCTTAGGCACATTAAGTGGATTCTGAGTAAAAGAAAGGGAA	2340
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Db	2341	CAGCAGGAGAAAGCTGTTTCGCTTGGTTCTGATTACCCAAATGAGCATGCTGGAAGGAGGT	2400
Qy	2401	TGTGAGGCTACGCTAAAACCTCTGCGTAGGGAGAGAGTACAGTGCATGAGTGTGGCGGCT	2460
Db	2401	TGTGAGGCTACGCTAAAACCTCTGCGTAGGGAGAGAGTACAGTGCATGAGTGTGGCGGCT	2460
Qy	2461	TTTGTCCACACTCGTGAAGGGTGAGTAATTCAGAGCCAATCACATCACAAGGATGGACAC	2520
Db	2461	TTTGTCCACACTCGTGAAGGGTGAGTAATTCAGAGCCAATCACATCACAAGGATGGACAC	2520
Qy	2521	ACCTAACTCATCACTTCAGGGGGAGATGAATGCTTTTCATGAGAAATTACACTCATAAGCT	2580
Db	2521	ACCTAACTCATCACTTCAGGGGGAGATGAATGCTTTTCATGAGAAATTACACTCATAAGCT	2580
Qy	2581	AAGCATCAGTTTTGAGTAAAATTTGAGTAGATGTTAAATATGAACATTTTATACCTCTTA	2640
Db	2581	AAGCATCAGTTTTGAGTAAAATTTGAGTAGATGTTAAATATGAACATTTTATACCTCTTA	2640
Qy	2641	CTAATGTCCCACCGACACCTTTTAATGTAAGCACATTTATTTATTAAGTTACTTGACATT	2700
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Qy	2701	AAATGCTTATGTCTGTATATTCTGTTTCATCCATCGATTTTCCCAAAAAGTAAGAGCATAG	2760
Db	2701	AAATGCTTATGTCTGTATATTCTGTTTCATCCATCGATTTTCCCAAAAAGTAAGAGCATAG	2760
Qy	2761	GAGATGAGGCCTACATGCCAAGAAAACATAAAATTTTACTCTTTAATTCTTACTTGAGCC	2820
Db	2761	GAGATGAGGCCTACATGCCAAGAAAACATAAAATTTTACTCTTTAATTCTTACTTGAGCC	2820
Qy	2821	AGCTTGTTGTTTATCAAGTGCTTTTTTGAAGAGACAGCACCTGTGAATTCTTCATTCTG	2880
Db	2821	AGCTTGTTGTTTATCAAGTGCTTTTTTGAAGAGACAGCACCTGTGAATTCTTCATTCTG	2880
Qy	2881	ATACAGTGTACCTTGTATTTAACATTTGTAATGTTGTTTCAAGTTTACATCTCTTTCAT	2940
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Qy	2941	TCTTTTATAGCAAATCAAACGTATTAGCTTCAGAAATTTATCAGAAGTTCATATATAAAT	3000
Db	2941	TCTTTTATAGCAAATCAAACGTATTAGCTTCAGAAATTTATCAGAAGTTCATATATAAAT	3000
Qy	3001	ATTTTGCAAAGGGTAAAAGGCTTTTTTGTTAAATAAAATAAAATTTATTATTTTCTTCTG	3060
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Qy	3061	ATGAATAGAGGCTCTTTTATGCTGCTGCTAATGAACCTAATTAGCTTTAAATTATCTCCT	3120
Db	3061	ATGAATAGAGGCTCTTTTATGCTGCTGCTAATGAACCTAATTAGCTTTAAATTATCTCCT	3120

Qy	3121	AGCAACATTGGTCACGTTTCAATCATGCTATTAGCAAAAAAAAAAA	3166
Db	3121	AGCAACATTGGTCACGTTTCAATCATGCTATTAGCAAAAAAAAAAA	3166

SCORE Search Results Details for Application 10501930 and Search Result us-10-501-930-1.rup.

[Score Home](#) [Retrieve Application](#) [SCORE System](#) [SCORE](#) [Comments /](#)
[Page](#) [List](#) [Overview](#) [FAQ](#) [Suggestions](#)

This page gives you Search Results detail for the Application 10501930 and Search Result us-10-501-930-1.rup.

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OM protein - protein search, using sw model

Run on: May 26, 2006, 23:22:24 ; Search time 302 Seconds
(without alignments)
1219.060 Million cell updates/sec

Title: US-10-501-930-1
Perfect score: 2102
Sequence: 1 MRSGGTLFALIGSLMLLLLL.....MLQLHMRGILKLQFSKCETA 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2102	100.0	398	1	SIA8F_MOUSE	Q8k4t1 mus musculu
2	2102	100.0	405	2	Q3T9N4_MOUSE	Q3t9n4 mus musculu
3	1936	92.1	398	2	Q6ZXC7_RAT	Q6zxc7 rattus norv
4	1922	91.4	362	2	Q8BI43_MOUSE	Q8bi43 mus musculu

5	1772	84.3	398	1	SIA8F_HUMAN	P61647	homo sapien
6	1772	84.3	398	2	Q5VZH4_HUMAN	Q5vzh4	homo sapien
7	1763	83.9	398	1	SIA8F_PANTR	P61648	pan troglod
8	1597	76.0	398	2	Q5NDG0_BOVIN	Q5ndg0	bos taurus
9	1183	56.3	398	2	Q6ZXC6_CHICK	Q6zxc6	gallus gall
10	728	34.6	343	2	Q6KC02_BRARE	Q6kc02	brachydanio
11	727.5	34.6	379	2	Q6KC00_TETNG	Q6kc00	tetraodon n
12	725.5	34.5	378	2	Q5K019_ORYLA	Q5k019	oryzias lat
13	719.5	34.2	372	2	Q50J40_FUGRU	Q50j40	fugu rubrip
14	719.5	34.2	379	2	Q6KC01_FUGRU	Q6kc01	fugu rubrip
15	715.5	34.0	356	2	Q6KBZ7_BRARE	Q6kbz7	brachydanio
16	710.5	33.8	342	2	P79783_CHICK	P79783	gallus gall
17	703	33.4	356	1	SIA8A_PANTR	P61642	pan troglod
18	702	33.4	342	2	Q78EI9_9MURI	Q78ei9	rattus sp.
19	701	33.3	356	2	P70554_RAT	P70554	rattus norv
20	700	33.3	356	1	SIA8A_HUMAN	Q92185	homo sapien
21	700	33.3	356	2	Q6ZXD2_BOVIN	Q6zxd2	bos taurus
22	700	33.3	412	1	SIA8E_MOUSE	P70126	mus musculu
23	699.5	33.3	370	2	Q6KBZ8_FUGRU	Q6kbz8	fugu rubrip
24	697	33.2	355	2	Q8BL76_MOUSE	Q8bl76	mus musculu
25	697	33.2	355	2	Q8K1C1_MOUSE	Q8klc1	mus musculu
26	692	32.9	376	2	Q3TRR3_MOUSE	Q3trr3	mus musculu
27	691	32.9	355	2	Q8BWI0_MOUSE	Q8bwi0	mus musculu
28	689	32.8	341	2	Q64468_MOUSE	Q64468	mus musculu
29	688	32.7	376	2	Q8JZQ3_MOUSE	Q8jzq3	mus musculu
30	687.5	32.7	359	2	Q6ZXA0_XENLA	Q6zxa0	xenopus lae
31	686	32.6	374	2	Q5NDF9_BOVIN	Q5ndf9	bos taurus
32	686	32.6	376	1	SIA8E_PANTR	P61646	pan troglod
33	686	32.6	376	2	Q6IAW7_HUMAN	Q6iaw7	homo sapien
34	686	32.6	376	2	Q6ZXC8_RAT	Q6zxc8	rattus norv
35	685	32.6	419	2	Q4SUV1_TETNG	Q4suv1	tetraodon n
36	682.5	32.5	338	2	Q6WRU1_XENLA	Q6wrul	xenopus lae
37	682	32.4	355	1	SIA8A_MOUSE	Q64687	mus musculu
38	678	32.3	376	2	Q6ZX98_CHICK	Q6zx98	gallus gall
39	677.5	32.2	345	2	Q6DNG6_XENTR	Q6dng6	xenopus tro
40	677	32.2	376	1	SIA8E_HUMAN	O15466	homo sapien
41	674.5	32.1	275	2	Q3V3B1_MOUSE	Q3v3b1	mus musculu
42	670	31.9	369	2	Q6KBZ9_FUGRU	Q6kbz9	fugu rubrip
43	665.5	31.7	268	2	Q50J35_BRARE	Q50j35	brachydanio
44	665.5	31.7	298	2	Q4T001_TETNG	Q4t001	tetraodon n
45	654.5	31.1	335	2	Q6KC12_TETNG	Q6kc12	tetraodon n

ALIGNMENTS

RESULT 1

SIA8F_MOUSE

ID SIA8F_MOUSE STANDARD; PRT; 398 AA.

AC Q8K4T1;

DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.

DT 01-OCT-2002, sequence version 1.

DT 07-FEB-2006, entry version 24.

DE Alpha-2,8-sialyltransferase 8F (EC 2.4.99.-) (ST8Sia VI).

GN Name=St8sia6; Synonyms=Siat8f;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA], AND CHARACTERIZATION.
RX MEDLINE=22086185; PubMed=11980897; DOI=10.1074/jbc.M112367200;
RA Takashima S., Ishida H.K., Inazu T., Ando T., Ishida H., Kiso M.,
RA Tsuji S., Tsujimoto M.;
RT "Molecular cloning and expression of a sixth type of alpha 2,8-
RT sialyltransferase (ST8Sia VI) that sialylates O-glycans.";
RL J. Biol. Chem. 277:24030-24038(2002).
CC -!- FUNCTION: Prefers O-glycans to N-glycans or glycolipids as
CC acceptor substrates. The minimal acceptor substrate is the NeuAc-
CC alpha-2,3(6)-Gal sequence at the nonreducing end of their
CC carbohydrate groups.
CC -!- PATHWAY: Glycosylation.
CC -!- SUBCELLULAR LOCATION: Golgi apparatus; Golgi membrane; single-pass
CC type II membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the glycosyltransferase 29 family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB059554; BAC01265.1; -; mRNA.
DR Ensembl; ENSMUSG00000003418; Mus musculus.
DR MGI; MGI:2386797; st8sia6.
DR GO; GO:0008373; F:sialyltransferase activity; IDA.
DR GO; GO:0016051; P:carbohydrate biosynthesis; IDA.
DR GO; GO:0009247; P:glycolipid biosynthesis; IDA.
DR GO; GO:0006493; P:protein amino acid O-linked glycosylation; IDA.
DR InterPro; IPR001675; Glyco_trans_29.
DR InterPro; IPR012163; Sialyl_trans.
DR Pfam; PF00777; Glyco_transf_29; 1.
DR PIRSF; PIRSF005557; Sialyl_trans; 1.
KW Glycoprotein; Glycosyltransferase; Golgi stack; Membrane;
KW Signal-anchor; Transferase; Transmembrane.
FT CHAIN 1 398 Alpha-2,8-sialyltransferase 8F.
FT /FTId=PRO_0000149300.
FT TOPO_DOM 1 3 Cytoplasmic (Potential).
FT TRANSMEM 4 24 Signal-anchor for type II membrane
FT protein (Potential).
FT TOPO_DOM 25 398 Lumenal (Potential).
FT CARBOHYD 66 66 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 93 93 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 151 151 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 196 196 N-linked (GlcNAc . . .) (Potential).
FT DISULFID 186 335 By similarity.
SQ SEQUENCE 398 AA; 45428 MW; A73A7A29640D4917 CRC64;

Query Match 100.0%; Score 2102; DB 1; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.5e-156;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRSGGTLFALIGSLMLLLLLRMLWCPADAPARSRLLEGSREDTSGTSAALKTLWSPTTP 60
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Db      1 MRSGGTLFALIGSLMLLLLLRMLWCPADAPARSRLLEGSREDTSGTSAALKTLWSPTTP 60

Qy     61 VPRTRNSTYLDEKTTQITEKCKDLQYSLNSLSNKTRRYSEDDYLQTITNIQRCPWNRQAE 120
        |||
Db     61 VPRTRNSTYLDEKTTQITEKCKDLQYSLNSLSNKTRRYSEDDYLQTITNIQRCPWNRQAE 120

Qy    121 EYDNFRAKLASCCDAIQDFVVSQNNTFVGTNMSYEVESEKKHIPIRENIFHMFVVSQPFVD 180
        |||
Db    121 EYDNFRAKLASCCDAIQDFVVSQNNTFVGTNMSYEVESEKKHIPIRENIFHMFVVSQPFVD 180

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Qy      181 YPYNQCAVVGNGGILNKSLCGAEIDKSDVFVRCNLPPITGSASKDVGSKTNLVTVNPSII 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 YPYNQCAVVGNGGILNKSLCGAEIDKSDVFVRCNLPPITGSASKDVGSKTNLVTVNPSII 240

Qy      241 TLKYQNLKEKKAQFLEDISTYGDAFLLLPAFSYRANTGISFKVYQTLKESKMRQKVLFFH 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TLKYQNLKEKKAQFLEDISTYGDAFLLLPAFSYRANTGISFKVYQTLKESKMRQKVLFFH 300

Qy      301 PRYLRLHALFWRTKGVTAYRLSTGLMIASVAVELCENVKLYGFWPFSKTIEDTPLSHHHY 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 PRYLRLHALFWRTKGVTAYRLSTGLMIASVAVELCENVKLYGFWPFSKTIEDTPLSHHHY 360

Qy      361 DNMLPKHGFHQMPKEYSQMLQLHMRGILKLQFSKCETA 398
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 DNMLPKHGFHQMPKEYSQMLQLHMRGILKLQFSKCETA 398
    
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RESULT 2

Q3T9N4_MOUSE

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ID  Q3T9N4_MOUSE  PRELIMINARY;  PRT;  405 AA.
AC  Q3T9N4;
DT  11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT  11-OCT-2005, sequence version 1.
DT  07-FEB-2006, entry version 5.
DE  Activated spleen cDNA, RIKEN full-length enriched library,
DE  clone:F830206C17 product:sialyltransferase 8 (alpha-2, 8-
DE  sialyltransferase) F, full insert sequence.
GN  Name=st8sia6;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muroidea; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=NOD; TISSUE=Activated spleen;
RX  MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA  Carninci P., Hayashizaki Y.;
RT  "High-efficiency full-length cDNA cloning.";
RL  Methods Enzymol. 303:19-44(1999).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=NOD; TISSUE=Activated spleen;
RX  PubMed=16141072; DOI=10.1126/science.1112014;
RA  Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA  Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA  Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA  Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA  Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA  Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA  Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA  Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA  di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA  Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA  Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA  Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA  Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA  Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA  Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA  Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA  Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
    
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RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of

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RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AK172400; BAE42986.1; -; mRNA.
 DR MGI; MGI:2386797; st8sia6.
 DR GO; GO:0008373; F:sialyltransferase activity; IDA.
 DR GO; GO:0016051; P:carbohydrate biosynthesis; IDA.
 DR GO; GO:0009247; P:glycolipid biosynthesis; IDA.
 DR GO; GO:0006493; P:protein amino acid O-linked glycosylation; IDA.
 DR InterPro; IPR001675; Glyco_trans_29.
 DR InterPro; IPR012163; Sialyl_trans.
 DR Pfam; PF00777; Glyco_transf_29; 1.
 DR PIRSF; PIRSF005557; Sialyl_trans; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 405 AA; 46323 MW; 48B7A17BE3443487 CRC64;

Query Match 100.0%; Score 2102; DB 2; Length 405;
 Best Local Similarity 100.0%; Pred. No. 2.5e-156;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSGGTLFALIGSLMLLLLLRLWCPADAPARSRLLEGSREDTSGTSAALKTLWSPTTP 60
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 Db 1 MRSGGTLFALIGSLMLLLLLRLWCPADAPARSRLLEGSREDTSGTSAALKTLWSPTTP 60
 Qy 61 VPTRNSTYLDEKTTQITEKCKDLQYSLNSLSNKTRRYSEDDYLQTITNIQRCPWNRQAE 120
 |||
 Db 61 VPTRNSTYLDEKTTQITEKCKDLQYSLNSLSNKTRRYSEDDYLQTITNIQRCPWNRQAE 120
 Qy 121 EYDNFRAKLASCCDAIQDFVVSQNNTPVGTNMSYEVESEKKHIPIRENIFHMFVSPQPFVD 180
 |||
 Db 121 EYDNFRAKLASCCDAIQDFVVSQNNTPVGTNMSYEVESEKKHIPIRENIFHMFVSPQPFVD 180
 Qy 181 YPYNQCAVVGNGGILNKSCLGAEIDKSDVFRCNLPPITGSASKDVGSKTNLVTVNPSII 240
 |||
 Db 181 YPYNQCAVVGNGGILNKSCLGAEIDKSDVFRCNLPPITGSASKDVGSKTNLVTVNPSII 240
 Qy 241 TLKYQNLKEKKAQFLEDISTYGDFAFLLLPAFSYRANTGISFKVYQTLKESKMRQKVLFFH 300
 |||
 Db 241 TLKYQNLKEKKAQFLEDISTYGDFAFLLLPAFSYRANTGISFKVYQTLKESKMRQKVLFFH 300
 Qy 301 PRYLRLHALFWRTKGVTAAYRLSTGLMIASVAVELCENVKLYGFWPFSKTIEDTPLSHHHY 360
 |||
 Db 301 PRYLRLHALFWRTKGVTAAYRLSTGLMIASVAVELCENVKLYGFWPFSKTIEDTPLSHHHY 360
 Qy 361 DNMLPKHGFHQMPKEYSQMLQLHMRGILKLQFSKCETA 398
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 Db 361 DNMLPKHGFHQMPKEYSQMLQLHMRGILKLQFSKCETA 398

RESULT 3
 Q6ZXC7_RAT
 ID Q6ZXC7_RAT PRELIMINARY; PRT; 398 AA.
 AC Q6ZXC7;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Alpha-2,8-sialyltransferase.
 GN Name=SIAT8F;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Rattus.